

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Artavanis-Tsakonas, S. et al.

(ii) TITLE OF INVENTION: Therapeutic And Diagnostic Methods
And Compositions Based On Notch Proteins And
Nucleic Acids

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Misrock, S. Leslie
(B) REGISTRATION NUMBER: 18,872
(C) REFERENCE/DOCKET NUMBER: 7326-015

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 142..2640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAAC ATTTGAGTAG TTGCCGCACA	60
CACACACACA CACAGCCGT GGATTATTAC ACTAAAAGCG ACACCTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171

Met His Trp Ile Lys Cys Leu Leu Thr Ala		
1 5 10		
TTC ATT TGC TTC ACA GTC ATC GTG CAG GTT CAC AGT TCC GGC AGC TTT	219	
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe		
15 20 25		
GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGG CGG GAC AAC GAG	267	
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu		
30 35 40		
GGT CGC TGC TGC AGC GGG GAG TCG GAC GGA GCG ACG GGC AAG TGC CTG	315	
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu		
45 50 55		
GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC	363	
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala		
60 65 70		
ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC	411	
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro		
75 80 85 90		
ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG	459	
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln		
95 100 105		
AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG	507	
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp		
110 115 120		
CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT	555	
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn		
125 130 135		
AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG	603	
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val		
140 145 150		
CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA	651	
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu		
155 160 165 170		
TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC	699	
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu		
175 180 185		
AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT	747	
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp		
190 195 200		
TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG	795	
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu		
205 210 215		
ACC GGA TGG CAG GGC GAT TAC TGT CAC ATA CCC AAA TGC GCC AAA GGC	843	
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly		
220 225 230		
TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG	891	
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu		
235 240 245 250		
GGC TGG AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC	939	
Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys		
255 260 265		

ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC ACC GGC GAG GGA TTG Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn 315 320 325 330	1131
GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly 335 340 345	1179
ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TCG GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 385 390	1323
TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371
AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro 415 420 425	1419
TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro 430 435 440	1467
GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu 445 450 455	1515
GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln 460 465 470	1563
TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser 475 480 485 490	1611
AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys 495 500 505	1659
TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr 510 515 520	1707
GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys 525 530 535	1755

CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val 540 545 550	1803
TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp 555 560 565 570	1851
TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg 575 580 585	1899
GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser 590 595 600	1947
GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys 605 610 615	1995
ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala 620 625 630	2043
AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly 635 640 645 650	2091
AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr 655 660 665	2139
GCG AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile 670 675 680	2187
AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala 685 690 695	2235
GCA GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly 700 705 710	2283
GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Ala Asn Ser Asp Phe 715 720 725 730	2331
TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr 735 740 745	2379
GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys 750 755 760	2427
GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT Gly Ala Ser Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser 765 770 775	2475
GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala 780 785 790	2523
GCG GCG GGA GTG GCC GGA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala 795 800 805 810	2571

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG	2619	
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val		
815	820	825
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670	
Val Cys Gly Thr Pro His Met		
830		
AAATCCGGAG AAATCCGCAT GGAGGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGTT	2730	
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTTG ATTGAAGCAG TTTAGTCGTC	2790	
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850	
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Trp Ile Lys Cys Leu Leu Thr Ala Phe Ile Cys Phe Thr Val			
1	5	10	15
Ile Val Gln Val His Ser Ser Gly Ser Phe Glu Leu Arg Leu Lys Tyr			
20	25	30	
Phe Ser Asn Asp His Gly Arg Asp Asn Glu Gly Arg Cys Cys Ser Gly			
35	40	45	
Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu Gly Ser Cys Lys Thr Arg			
50	55	60	
Phe Arg Val Cys Leu Lys His Tyr Gln Ala Thr Ile Asp Thr Thr Ser			
65	70	75	80
Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro Ile Leu Gly Glu Asn Ser			
85	90	95	
Val Asn Leu Thr Asp Ala Gln Arg Phe Gln Asn Lys Gly Phe Thr Asn			
100	105	110	
Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp Pro Gly Thr Phe Ser Leu			
115	120	125	
Ile Val Glu Ala Trp His Asp Thr Asn Asn Ser Gly Asn Ala Arg Thr			
130	135	140	
Asn Lys Leu Leu Ile Gln Arg Leu Leu Val Gln Gln Val Leu Glu Val			
145	150	155	160
Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu Ser Gln Tyr Thr Ser Leu			
165	170	175	
Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly			
180	185	190	
Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr			
195	200	205	

Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp
210 215 220

Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
225 230 235 240

Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
245 250 255

Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
260 265 270

Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
275 280 285

Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly
290 295 300

Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala
305 310 315 320

Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp
325 330 335

Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro
340 345 350

His Thr Lys Thr Gly Tyr Lys Cys His Cys Ala Asn Gly Trp Ser Gly
355 360 365

Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His
370 375 380

Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln
385 390 395 400

Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp
405 410 415

Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser
420 425 430

Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ala Gly Phe Ser Gly Thr
435 440 445

Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn
450 455 460

Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val
465 470 475 480

Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu
485 490 495

Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp
500 505 510

Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val
515 520 525

Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys
530 535 540

Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg
545 550 555 560

Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala

565

570

575

His Gln Tyr Gly Ala Thr Thr Gln Ala Arg Ala Asp Gly Leu Thr Asn
580 585 590

Ala Gln Val Val Leu Ile Ala Val Phe Ser Val Ala Met Pro Leu Val
595 600 605

Ala Val Ile Ala Ala Cys Val Val Phe Cys Met Lys Arg Lys Arg Lys
610 615 620

Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala Arg Lys Gln Asn Glu Gln
625 630 635 640

Asn Ala Val Ala Thr Met His His Asn Gly Ser Gly Val Gly Val Ala
645 650 655

Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr Gly Ser Asn Ser Gly Leu
660 665 670

Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile Lys Asn Thr Trp Asp Lys
675 680 685

Ser Val Asn Asn Ile Cys Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala
690 695 700

Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly Gly Tyr Val Ala Ser Val
705 710 715 720

Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe Cys Val Ala Pro Leu Gln
725 730 735

Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr Asp Pro Thr Leu Met His
740 745 750

Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys Gly Ala Ser Gly Gly Gly
755 760 765

Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser Val Leu Gly Glu Gly Ser
770 775 780

Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala Ala Gly Val Ala Gly
785 790 795 800

Ala Cys Ser Ser Gln Leu Met Ala Ala Ala Ser Ala Ala Gly Ser Gly
805 810 815

Ala Gly Thr Ala Gln Gln Gln Arg Ser Val Val Cys Gly Thr Pro His
820 825 830

Met

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 442..1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCTT TTCTGTCAAC GCTAAAGATC	60
TACAAAACAT CAGCGCCTAT CAAGTGGAAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
CCAAAATCTG CATAATGGG CTAATTAAGG CTGCCCAGCG AATTTACATT TGTGTGGTGC	360
CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA	471
Met Phe Arg Lys His Phe Arg Arg Lys Pro	
1 5 10	
GCT ACG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG	519
Ala Thr Ser Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu	
15 20 25	
GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG	567
Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg	
30 35 40	
GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA	615
Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser	
45 50 55	
TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC	663
Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Leu Val	
60 65 70	
CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711
His Lys Ile Ser Ala Ala Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile	
75 80 85 90	
TCA AAT ACC AAC AGC CAT CTA CTC AAC GGC TAT TGC TGC GGC ATG CCA	759
Ser Asn Thr Asn Ser His Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro	
95 100 105	
GCG GAA CTT AGG GCC ACC AAG ACG ATA GGC TGC TCG CCA TGC ACG ACG	807
Ala Glu Leu Arg Ala Thr Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr	
110 115 120	
GCA TTC CGG CTG TGC CTG AAG GAG TAC CAG ACC ACG GAG CAG GGT GCC	855
Ala Phe Arg Leu Cys Leu Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala	
125 130 135	
AGC ATA TCC ACG GGC TGT TCG TTT GGC AAC GCC ACC ACC AAG ATA CTG	903
Ser Ile Ser Thr Gly Cys Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu	
140 145 150	
GGT GGC TCC AGC TTT GTG CTC AGC GAT CCG GGT GTG GGA GCC ATT GTG	951
Gly Gly Ser Ser Phe Val Leu Ser Asp Pro Gly Val Gly Ala Ile Val	
155 160 165 170	
CTG CCC TTT ACG TTT CGT TGG ACG AAG TCG TTT ACG CTG ATA CTG CAG	999
Leu Pro Phe Thr Phe Arg Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln	
175 180 185	
GCG TTG GAT ATG TAC AAC ACA TCC TAT CCA GAT GCG GAG AGG TTA ATT	1047

Ala Leu Asp Met Tyr Asn Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile		
190	195	200
GAG GAA ACA TCA TAC TCG GGC GTG ATA CTG CCG TCG CCG GAG TGG AAG		1095
Glu Glu Thr Ser Tyr Ser Gly Val Ile Leu Pro Ser Pro Glu Trp Lys		
205	210	215
ACG CTG GAC CAC ATC GGG CGG AAC GCG CGG ATC ACC TAC CGT GTC CGG		1143
Thr Leu Asp His Ile Gly Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg		
220	225	230
GTG CAA TGC GCC GTT ACC TAC TAC AAC ACG ACC TGC ACG ACC TTC TGC		1191
Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Cys Thr Phe Cys		
235	240	245
250		
CGT CCG CGG GAC GAT CAG TTC GGT CAC TAC GCC TGC GGC TCC GAG GGT		1239
Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu Gly		
255	260	265
CAG AAG CTC TGC CTG AAT GGC TGG CAG GGC GTC AAC TGC GAG GAG GCC		1287
Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys Glu Glu Ala		
270	275	280
ATA TGC AAG GCG GGC TGC GAC CCC GTC CAC GGC		
Ile Cys Lys Ala Gly Cys Asp Pro Val His Gly		
285	290	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Arg Lys His Phe Arg Arg Lys Pro Ala Thr Ser Ser Ser Leu		
1	5	10
15		
Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu Gly Met Ser Lys Lys Thr		
20	25	30
Ala Thr Lys Arg Gln Arg Pro Arg His Arg Val Pro Lys Ile Ala Thr		
35	40	45
Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser Leu Lys Ser Ala Cys Asn		
50	55	60
Leu Ile Ala Leu Ile Leu Ile Leu Val His Lys Ile Ser Ala Ala		
65	70	75
80		
Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile Ser Asn Thr Asn Ser His		
85	90	95
Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro Ala Glu Leu Arg Ala Thr		
100	105	110
Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr Ala Phe Arg Leu Cys Leu		
115	120	125
Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala Ser Ile Ser Thr Gly Cys		
130	135	140
Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu Gly Gly Ser Ser Phe Val		

145	150	155	160
Leu Ser Asp Pro Gly Val Gly Ala Ile Val Leu Pro Phe Thr Phe Arg			
165	170	175	
Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln Ala Leu Asp Met Tyr Asn			
180	185	190	
Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser			
195	200	205	
Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly			
210	215	220	
Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr			
225	230	235	240
Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln			
245	250	255	
Phe Gly His Tyr Ala Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn			
260	265	270	
Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys			
275	280	285	
Asp Pro Val His Gly			
290			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCTCGGGAA CGGGGGGTAA CACTGAAAGG	60
TCGAGTACCC ATTTCCGTCA TAACGGGTTG GTCGCCCCCT AGGGGTCGGA GTCAGGTGGA	120
CGGGGAGGTGCG ACAACGCCCCG GGGGACGGGT GGTACATGGT GTAAGGTCTT TACCGGACCG	180
GGCAAACGGG TCACACCGAA AGGGGTGAAC GGTAAC TACG GGGTCGTCCCT GCCCGTCCAT	240
CGAGTCTGGT AAGAGGGTCG CCTTAAG	267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCCTTC CATTATACGT GACTTTCTG AAACCTGTAGC CACCCCTAGTG TCTCTAACTC	60
CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
GCGGGCATGC TCCAGTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
AACCCGGAAC TGAAGGCTGG CTCTCACCCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC	300
GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACAA	360
TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
GGCACGTGAT GCCAAGGTGT ATTCAAGATCT GTTA	574

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCAGATTCT GATTTCGCAAC CGAGTAAC TG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
CTGTCAATAA TGTGGAGGCA ACTCTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC	240
AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCG GGAGGAGCTA TAAGC	295

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCATT CAGGAGGAAA GGGTGGGGAG AGAACGAGGC ACCCACTTTC CCGTGGCTGG	60
ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGG CGGAGTGCCA	120
TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180

GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG	240
CAGAGCTG	248

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTNNA GTCGGAGGGA CATTGTCG	60
ACCAAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG	120
GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACGTAAAC CTCCGGTCGA CAGTCGGTAA	180
GCGAACAAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG	240
CGGCCTTAAG GACGTGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GGCGCCACCT	300
CGAGGNCGAA AACAAAGGGAA ATC	323

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC	48
Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn	
1 5 10 15	
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC	96
His Ala Cys Gly Trp Asp Gly Asp Cys Ser Leu Asn Phe Asn Asp	
20 25 30	
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT	144
Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser	
35 40 45	
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC	192
Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp	
50 55 60	
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC	240

Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp	65	70	75	80	
CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys	85	90	95		288
AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val	100	105	110		336
CCC GAG AGG CTG GCG GCC GGC ACG CTG GTG GTG GTG GTG CTG ATG CCG Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro	115	120	125		384
CCG GAG CAG CTG CGC AAC AGC TCC TTC CAC TTC CTG CGG GAG CTC AGC Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser	130	135	140		432
CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln	145	150	155	160	480
CAG ATG ATC TTC CCC TAC TAC GGC CGC GAG GAG GAG CTG CGC AAG CAC Gln Met Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His	165	170	175		528
CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG Pro Ile Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu	180	185	190		576
GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG Gly Gln Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg	195	200	205		624
CGG CGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC Arg Arg Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr	210	215	220		672
CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC Leu Glu Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe	225	230	235	240	720
CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu	245	250	255		768
GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GGC GTG CAG AGT GAG ACC Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr	260	265	270		816
GTG GAG CCG CCC CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG Val Glu Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala	275	280	285		864
GCC GCC TTT GTG CTT CTG TTC GTG GGC TGC GGG GTG CTG CTG TCC Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser	290	295	300		912
CGC AAG CGC CGG CGG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe	305	310	315	320	960
AAA GTG TCT GAG GCC AGC AAG AAG CGG CGG GAG CCC CTC GGC GAG Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu	325	330	335		1008

GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu 340 345 350	1056
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys 355 360 365	1104
AAG TTC CCG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln 370 375 380	1152
ACA GAC CAC CGG CAG TGG ACT CAG CAG CAC CTG GAT GCC GCT GAC CTG Thr Asp His Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu 385 390 395 400	1200
CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC Arg Met Ser Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala 405 410 415	1248
GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC Asp Cys Met Asp Val Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu 420 425 430	1296
ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG Met Ile Ala Ser Cys Ser Gly Gly Leu Glu Thr Gly Asn Ser Glu 435 440 445	1344
GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC Glu Glu Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly 450 455 460	1392
GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC Ala Ser Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His 465 470 475 480	1440
CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG Leu Ala Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu 485 490 495	1488
GCC AGC GCA GAT GCC AAC ATC CAG GAC AAC ATG GGC CGC ACC CCG CTG Ala Ser Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu 500 505 510	1536
CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC His Ala Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile 515 520 525	1584
CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG Arg Asn Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr 530 535 540	1632
CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu Asp 545 550 555 560	1680
CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG Leu Ile Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu Gly Lys 565 570 575	1728
TCC GCC CTG CAC TGG GCC GCC GTG AAC AAT GTG GAT GCC GCA GTT Ser Ala Leu His Trp Ala Ala Val Asn Asn Val Asp Ala Ala Val 580 585 590	1776
GTC CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG Val Leu Leu Lys Asn Gly Ala Asn Lys Asp Met Gln Asn Asn Arg Glu 595 600 605	1824

GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCC Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala 610 615 620	1872
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG Lys Val Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met 625 630 635 640	1920
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC Asp Arg Leu Pro Arg Asp Ile Ala Gln Glu Arg Met His His Asp Ile 645 650 655	1968
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC Val Arg Leu Leu Asp Glu Tyr Asn Leu Val Arg Ser Pro Gln Leu His 660 665 670	2016
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG Gly Ala Pro Leu Gly Gly Thr Pro Thr Leu Ser Pro Pro Leu Cys Ser 675 680 685	2064
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG Pro Asn Gly Tyr Leu Gly Ser Leu Lys Pro Gly Val Gln Gly Lys Lys 690 695 700	2112
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC Val Arg Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala 705 710 715 720	2160
AAG GAC CTC AAG GCA CGG AGG AAG TCC CAG GAT GGC AAG GGC TGC Lys Asp Leu Lys Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys 725 730 735	2208
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA Leu Leu Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser 740 745 750	2256
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC Pro His Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser 755 760 765	2304
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG Pro Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met 770 775 780	2352
CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro 785 790 795 800	2400
GAG ATG GCG GCG CTG GGT GGG GGC CGG CTG GCC TTT GAG ACT GGC Glu Met Ala Ala Leu Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly 805 810 815	2448
CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val 820 825 830	2496
CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC Leu Gly Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser 835 840 845	2544
ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly 850 855 860	2592
ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC Met Val Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly 865 870 875 880	2640

CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro 885 890 895	2688
CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr 900 905 910	2736
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln 915 920 925	2784
ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG AAC CTG Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Asn Leu 930 935 940	2832
CAG CCA GCA AAC ATC CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA Gln Pro Ala Asn Ile Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro 945 950 955 960	2880
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu 965 970 975	2928
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro 980 985 990	2976
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser 995 1000 1005	3024
CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr 1010 1015 1020	3072
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro 1025 1030 1035 1040	3120
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met 1045 1050 1055	3168
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile 1060 1065 1070	3216
GAA GCT CCC GAC TCA TGG Glu Ala Pro Asp Ser Trp 1075	3234

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1078 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
1 5 10 15

His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
20 25 30

Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
35 40 45

Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
50 55 60

Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp
65 70 75 80

Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys
85 90 95

Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val
100 105 110

Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro
115 120 125

Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser
130 135 140

Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln
145 150 155 160

Gln Met Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His
165 170 175

Pro Ile Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu
180 185 190

Gly Gln Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg
195 200 205

Arg Arg Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr
210 215 220

Leu Glu Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe
225 230 235 240

Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu
245 250 255

Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr
260 265 270

Val Glu Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala
275 280 285

Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser
290 295 300

Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe
305 310 315 320

Lys Val Ser Glu Ala Ser Lys Lys Arg Arg Glu Pro Leu Gly Glu
325 330 335

Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu
340 345 350

Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys
355 360 365

Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln

370	375	380
Thr Asp His Arg Gln Trp	Thr Gln Gln His	Leu Asp Ala Ala Asp Leu
385	390	395
400		
Arg Met Ser Ala Met Ala Pro	Thr Pro Pro Gln Gly	Glu Val Asp Ala
405	410	415
Asp Cys Met Asp Val Asn Val Arg	Gly Pro Asp Gly	Phe Thr Pro Leu
420	425	430
Met Ile Ala Ser Cys Ser Gly	Gly Leu Glu Thr Gly	Asn Ser Glu
435	440	445
Glu Glu Glu Asp Ala Pro Ala Val	Ile Ser Asp Phe Ile	Tyr Gln Gly
450	455	460
Ala Ser Leu His Asn Gln Thr Asp Arg	Thr Gly Glu Thr Ala	Leu His
465	470	475
480		
Leu Ala Ala Arg Tyr Ser Arg Ser Asp	Ala Ala Lys Arg Leu	Leu Glu
485	490	495
Ala Ser Ala Asp Ala Asn Ile Gln Asp Asn Met	Gly Arg Thr Pro Leu	
500	505	510
His Ala Ala Val Ser Ala Asp Ala Gln Gly	Val Phe Gln Ile Leu	Ile
515	520	525
Arg Asn Arg Ala Thr Asp Leu Asp Ala Arg	Met His Asp Gly	Thr Thr
530	535	540
Pro Leu Ile Leu Ala Ala Arg Leu Ala Val	Glu Gly Met Leu Glu	Asp
545	550	555
560		
Leu Ile Asn Ser His Ala Asp Val Asn Ala Val	Asp Asp Leu Gly	Lys
565	570	575
Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn	Val Asp Ala Ala Val	
580	585	590
Val Leu Leu Lys Asn Gly Ala Asn Lys Asp Met	Gln Asn Asn Arg Glu	
595	600	605
Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu	Gly Ser Tyr Glu Thr Ala	
610	615	620
Lys Val Leu Leu Asp His Phe Ala Asn Arg	Asp Ile Thr Asp His	Met
625	630	635
640		
Asp Arg Leu Pro Arg Asp Ile Ala Gln Glu	Arg Met His His Asp Ile	
645	650	655
Val Arg Leu Leu Asp Glu Tyr Asn Leu Val	Arg Ser Pro Gln Leu	His
660	665	670
Gly Ala Pro Leu Gly Gly Thr	Pro Thr Leu Ser Pro	Pro Leu Cys Ser
675	680	685
Pro Asn Gly Tyr Leu Gly Ser Leu Lys	Pro Gly Val Gln Gly	Lys Lys
690	695	700
705		
Val Arg Lys Pro Ser Ser Lys Gly Leu Ala	Cys Gly Ser Lys Glu	Ala
710	715	720
Lys Asp Leu Lys Ala Arg Arg Lys Lys	Ser Gln Asp Gly	Lys Gly Cys
725	730	735

Leu Leu Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser
740 745 750

Pro His Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser
755 760 765

Pro Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met
770 775 780

Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro
785 790 795 800

Glu Met Ala Ala Leu Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly
805 810 815

Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val
820 825 830

Leu Gly Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser
835 840 845

Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly
850 855 860

Met Val Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly
865 870 875 880

Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro
885 890 895

Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr
900 905 910

Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln
915 920 925

Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu
930 935 940

Gln Pro Ala Asn Ile Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro
945 950 955 960

Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu
965 970 975

Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro
980 985 990

Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser
995 1000 1005

Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr
1010 1015 1020

Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro
1025 1030 1035 1040

Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met
1045 1050 1055

Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile
1060 1065 1070

Glu Ala Pro Asp Ser Trp
1075

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..1972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys 1 5 10 15	46
ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 30	94
GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	238
AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met 80 85 90 95	286
GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val 100 105 110	334
TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430
GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val 145 150 155	478
GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Val Asn Asn 160 165 170 175	526
GTG GAG GCA ACT CTT TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG Val Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met 180 185 190	574
CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly 195 200 205	622

AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp 210 215 220	670
ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg 225 230 235	718
ATG CAC CAT GAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro 240 245 250 255	766
AGC CCT CCA GGC ACC GTG TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys 260 265 270	814
GGG CCC AAC AGA TCT TTC CTC AGC CTG AAG CAC ACC CCA ATG GGC AAG Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys 275 280 285	862
AAG TCT AGA CGG CCC AGT GCC AAG AGT ACC ATG CCT ACT AGC CTC CCT Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro 290 295 300	910
AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GGT AGT AGG AGG AAG AAG Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys 305 310 315	958
TCT CTG AGT GAG AAG GTC CAA CTG TCT GAG AGT TCA GTA ACT TTA TCC Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser 320 325 330 335	1006
CCT GTT GAT TCC CTA GAA TCT CCT CAC ACG TAT GTT TCC GAC ACC ACA Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr 340 345 350	1054
TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn 355 360 365	1102
CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His 370 375 380	1150
GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGG Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly 385 390 395	1198
GCC AGC ACT GTG CTT CCC TCA GTG AGC CAG TTG CTA TCC CAC CAC CAC Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His 400 405 410 415	1246
ATT GTG TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His 420 425 430	1294
CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG GAG GTG AAT GAG Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu 435 440 445	1342
ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTG GCT CCA GCT GAG GGC Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly 450 455 460	1390
ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT GAA GGG AAG CAC Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His 465 470 475	1438

ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu 480 485 490 495	1486
ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln 500 505 510	1534
TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln 515 520 525	1582
ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met 530 535 540	1630
ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser 580 585 590	1774
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser 595 600 605	1822
CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAGA TGTCTTATT CAGATAATGC AAGAGAAGCA ATTGTCAGT	2142
TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAACTCT AATAAGACAA GTTTGTGGAA	2202
ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTTACTCTC TTCTATTGG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCTG TTGGGAATTA TGCCCTGGAA	2382
TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTGT CTTCATTGG	2442
TGCTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC	2502
CTTGTGCTT TTGATCATTG TGGCCCATGA AAGCAACTTT GGTCTCCTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCACAAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC	2622

TTTCAAGTAT GTTGTTCCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT	2682
CATTCCCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAAATTTG GGGGCAGGAG	2742
ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT	2802
TTACCAGGAA GAAGGGTGTG AGTTTGTGT TTTTCTGTGT ATGGGCCTGG TCAGTGAAA	2862
GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTAAAAA CCAGAAAAAG	2922
GTTTCCAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT	3042
CCAGATCTG AGCATTCTAG GCCTGTTCA CTCACTCACC CAGCATATGA AACTAGTCTT	3102
AACTGTTGAG CCTTTCCCTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCCTG	3162
CCATTTAGGA CTGAACCTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTGT	3222
CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTCTT	3282
TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT	3342
TTATATGTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC	3402
CTATAAGAAG GTTGGAAAAG GAGGAACATAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT	3462
TTCTTTCCCT CTGAAGCGGC CATGACATTC CCTTGGCAA CTAACGTAGA AACTCAACAG	3522
AACATTTCC TTTCCTAGAG TCACCTTTA GATGATAATG GACAACATA GACTTGCTCA	3582
TTGTTCAGAC TGATTGCCCT TCACCTGAAT CCACTCTCTG TATTCTATGCT CTTGGCAATT	3642
TCTTGACTT TCTTTTAAGG GCAGAACAT TTTAGTTAAT TGTAGATAAA GAATAGTTT	3702
CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC	3762
AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT	3822
AACAGGTGAA TTCCCGACTC TTTGGTTTG AATGACAGTT CTCATTCTT CTATGGCTGC	3882
AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC	3942
CCTGCGTGTGTC TGTTGGCATA ATAGTTACA AATGGTTTT TCAGTCCTAT CCAAATTAT	4002
TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC	4062
TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT	4122
TATCATTCTA AATGGTGACT CTCTGCCCT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGACCCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GCGATGGCGA TGACTTTCTT CCCCTG	4268

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr
1 5 10 15

Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp
20 25 30

Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu
35 40 45

Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu
50 55 60

Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys
65 70 75 80

Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly
85 90 95

Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe
100 105 110

Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn
115 120 125

Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly
130 135 140

Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp
145 150 155 160

Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val
165 170 175

Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln
180 185 190

Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser
195 200 205

Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp Ile
210 215 220

Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg Met
225 230 235 240

His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro Ser
245 250 255

Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys Gly
260 265 270

Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys Lys
275 280 285

Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro Asn
290 295 300

Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys Ser
305 310 315 320

Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser Pro
325 330 335

Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr Ser
340 345 350

Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn Pro

355	360	365
Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His Ala		
370	375	380
Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly Ala		
385	390	395
Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His Ile		
405	410	415
Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His Pro		
420	425	430
Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu Thr		
435	440	445
Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly Thr		
450	455	460
His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His Ile		
465	470	475
480		
Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu Ile		
485	490	495
Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln Ser		
500	505	510
Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln Ile		
515	520	525
Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met Met		
530	535	540
Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr His		
545	550	555
560		
Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln His		
565	570	575
Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser Gly		
580	585	590
His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser Pro		
595	600	605
Asp Gln Trp Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser Asp		
610	615	620
Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gln Arg Gly		
625	630	635
640		
Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val Tyr		
645	650	655
Ala		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu	Asp	Ile	Asp	Glu	Cys	Asp	Gln	Gly	Ser	Pro	Cys	Glu	His	Asn	Gly
1				5					10					15	
Ile	Cys	Val	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Asn	Cys	Ser	Gln	Gly
	20						25						30		
Phe	Thr	Gly	Pro	Arg	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Glu	Ser	His
	35					40						45			
Pro	Cys	Gln	Asn	Glu	Gly	Ser	Cys	Leu	Asp	Asp	Pro	Gly	Thr	Phe	Arg
	50				55						60				
Cys	Val	Cys	Met	Pro	Gly	Phe	Thr	Gly	Thr	Gln	Cys	Glu			
	65				70				75						

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Asp	Val	Asp	Glu	Cys	Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu	His	Gly
1				5					10				15		
Gly	Arg	Cys	Thr	Asn	Thr	Leu	Gly	Ser	Phe	Gln	Cys	Asn	Cys	Pro	Gln
	20						25					30			
Gly	Tyr	Ala	Gly	Pro	Arg	Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Leu	Ser
	35					40					45				
Asn	Pro	Cys	Gln	Asn	Asp	Ser	Thr	Cys	Leu	Asp	Gln	Ile	Gly	Glu	Phe
	50					55					60				
Gln	Cys	Ile	Cys	Met	Pro	Gly	Tyr	Glu	Gly	Leu	Tyr	Cys	Glu		
	65					70			75						

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr	Pro	Pro	Gln	Gly	Glu	Ile	Glu	Ala	Asp	Cys	Met	Asp	Val	Asn	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1	5	10	15												
Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	Met	Ile	Ala	Ser	Cys	Ser	Gly
				20				25					30		
Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Ser	Ala
		35				40						45			
Asn	Met	Ile	Ser	Asp	Phe	Ile	Gly	Gln	Gly	Ala	Gln	Leu	His	Asn	Gln
	50					55				60					
Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ala
	65				70				75				80		
Arg	Ala	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Ser	Ser	Ala	Asp	Ala	Asn
					85				90			95			
Val	Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu	His	Ala	Ala	Val	Ala	Ala
				100				105				110			
Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Ala	Thr	Asp
		115				120				125					
Leu	Asp	Ala	Arg	Met	Phe	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala
		130				135				140					
Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Glu	Glu	Leu	Ile	Asn	Ala	His	Ala
		145				150				155			160		
Asp	Val	Asn	Ala	Val	Asp	Glu	Phe	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala
				165				170			175				
Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Ala	Val	Leu	Leu	Lys	Asn	Ser
				180				185			190				
Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Lys	Glu	Glu	Thr	Ser	Leu	Phe	Leu
		195				200			205						
Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His
		210				215			220						
Tyr	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp
		225				230			235			240			
Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	His	Leu	Leu	Asp	Glu
				245				250			255				
Tyr	Asn	Leu	Val	Lys	Ser	Pro	Thr	Leu	His	Asn	Gly	Pro	Leu	Gly	Ala
				260				265			270				
Thr	Thr	Leu	Ser	Pro	Pro	Ile	Cys	Ser	Pro	Asn	Gly	Tyr	Met	Gly	Asn
				275				280			285				
Met	Lys	Pro	Ser	Val	Gln	Ser	Lys	Lys	Ala	Arg	Lys	Pro	Ser	Ile	Lys
				290				295			300				
Gly	Asn	Gly	Cys	Lys	Glu	Ala	Lys	Glu	Leu	Lys	Ala	Arg	Arg	Lys	Lys
				305				310			315			320	
Ser	Gln	Asp	Gly	Lys	Thr	Thr	Leu	Leu	Asp	Ser	Gly	Ser	Ser	Gly	Val
				325				330			335				
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Thr	His	Gly	Tyr	Leu	Ser	Asp
				340				345			350				
Val	Ser	Ser	Pro	Pro	Leu	Met	Thr	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser
				355				360			365				

Met Pro Leu Asn His Leu Thr Ser Met Pro Glu Ser Gln Leu Gly Met
370 375 380

Asn His Ile Asn Met Ala Thr Lys Gln Glu Met Ala Ala Gly Ser Asn
385 390 395 400

Arg Met Ala Phe Asp Ala Met Val Pro Arg Leu Thr His Leu Asn Ala
405 410 415

Ser Ser Pro Asn Thr Ile Met Ser Asn Gly Ser Met His Phe Thr Val
420 425 430

Gly Gly Ala Pro Thr Met Asn Ser Gln Cys Asp Trp Leu Ala Arg Leu
435 440 445

Gln Asn Gly Met Val Gln Asn Gln Tyr Asp Pro Ile Arg Asn Gly Ile
450 455 460

Gln Gln Gly Asn Ala Gln Gln Ala Gln Ala Leu Gln His Gly Leu Met
465 470 475 480

Thr Ser Leu His Asn Gly Leu Pro Ala Thr Thr Leu Ser Gln Met Met
485 490 495

Thr Tyr Gln Ala Met Pro Asn Thr Arg Leu Ala Asn Gln Pro His Leu
500 505 510

Met Gln Ala Gln Gln Met Gln Gln Gln Asn Leu Gln Leu His Gln
515 520 525

Ser Met Gln Gln Gln His His Asn Ser Ser Thr Thr Ser Thr His Ile
530 535 540

Asn Ser Pro Phe Cys Ser Ser Asp Ile Ser Gln Thr Asp Leu Gln Gln
545 550 555 560

Met Ser Ser Asn Asn Ile His Ser Val Met Pro Gln Asp Thr Gln Ile
565 570 575

Phe Ala Ala Ser Leu Pro Ser Asn Leu Thr Gln Ser Met Thr Thr Ala
580 585 590

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Met Asp
595 600 605

Asn Thr Pro Ser His Gln Leu Gln Val Pro Asp His Pro Phe Leu Thr
610 615 620

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Pro His Ser
625 630 635 640

Asn Met Ser Asp Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr
645 650

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
1 5 10 15

Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
20 25 30

Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Asp Ala Pro Ala
35 40 45

Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
50 55 60

Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
65 70 75 80

Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
85 90 95

Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
100 105 110

Ala Gln Gly Val Phe Gln Ile Leu Leu Arg Asn Arg Ala Thr Asp Leu
115 120 125

Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
130 135 140

Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
145 150 155 160

Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
165 170 175

Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
180 185 190

Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala
195 200 205

Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
210 215 220

Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
225 230 235 240

Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
245 250 255

Asn Leu Val Arg Ser Pro Gln Leu His Gly Thr Ala Leu Gly Gly Thr
260 265 270

Pro Thr Leu Ser Pro Thr Leu Cys Ser Pro Asn Gly Tyr Leu Gly Asn
275 280 285

Leu Lys Ser Ala Thr Gln Gly Lys Lys Ala Arg Lys Pro Ser Thr Lys
290 295 300

Gly Leu Ala Cys Ser Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
305 310 315 320

Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Ser Met
325 330 335

Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Gly Tyr Leu Ser Asp
340 345 350

Val Ala Ser Pro Pro Leu Pro Ser Pro Phe Gln Gln Ser Pro Ser Met

355	360	365
Pro Leu Ser His Leu Pro Gly Met Pro Asp Thr His Leu Gly Ile Ser		
370	375	380
His Leu Asn Val Ala Ala Lys Pro Glu Met Ala Ala Leu Ala Gly Gly		
385	390	395
		400
Ser Arg Leu Ala Phe Glu Pro Pro Pro Arg Leu Ser His Leu Pro		
405	410	415
Val Ala Ser Ser Ala Ser Thr Val Leu Ser Thr Asn Gly Thr Gly Ala		
420	425	430
Met Asn Phe Thr Val Gly Ala Pro Ala Ser Leu Asn Gly Gln Cys Glu		
435	440	445
Trp Leu Pro Arg Leu Gln Asn Gly Met Val Pro Ser Gln Tyr Asn Pro		
450	455	460
Leu Arg Pro Gly Val Thr Pro Gly Thr Leu Ser Thr Gln Ala Ala Gly		
465	470	475
		480
Leu Gln His Gly Met Met Ser Pro Ile His Ser Ser Leu Ser Thr Asn		
485	490	495
Thr Leu Ser Pro Ile Ile Tyr Gln Gly Leu Pro Asn Thr Arg Leu Ala		
500	505	510
Thr Gln Pro His Leu Val Gln Thr Gln Gln Val Gln Pro Gln Asn Leu		
515	520	525
Gln Ile Gln Pro Gln Asn Leu Gln Pro Pro Ser Gln Pro His Leu Ser		
530	535	540
Val Ser Ser Ala Ala Asn Gly His Leu Gly Arg Ser Phe Leu Ser Gly		
545	550	555
		560
Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly Pro Ser Ser Leu Pro		
565	570	575
Val His Thr Ile Leu Pro Gln Glu Ser Gln Ala Leu Pro Thr Ser Leu		
580	585	590
Pro Ser Ser Met Val Pro Pro Met Thr Thr Thr Gln Phe Leu Thr Pro		
595	600	605
Pro Ser Gln His Ser Tyr Ser Ser Ser Pro Val Asp Asn Thr Pro Ser		
610	615	620
His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu		
625	630	635
		640
Ser Pro Asp Gln Trp Ser Ser Ser Arg His Ser Asn Ile Ser Asp		
645	650	655
Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr		
660	665	

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
1 5 10 15

Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
20 25 30

Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Asp Ala Pro Ala
35 40 45

Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
50 55 60

Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
65 70 75 80

Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
85 90 95

Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
100 105 110

Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp Leu
115 120 125

Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
130 135 140

Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
145 150 155 160

Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
165 170 175

Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
180 185 190

Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr Pro Leu Phe Leu Ala
195 200 205

Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
210 215 220

Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
225 230 235 240

Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
245 250 255

Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala Pro Leu Gly Gly Thr
260 265 270

Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly Tyr Leu Gly Ser
275 280 285

Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg Lys Pro Ser Ser Lys
290 295 300

Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
305 310 315 320

Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Gly Met

325	330	335	
Leu Ser Pro Val Asp Ser Leu Glu	Ser Pro His Gly Tyr	Leu Ser Asp	
340 345	350		
Val Ala Ser Pro Pro Leu Leu Pro	Ser Pro Phe Gln Gln	Ser Pro Ser	
355	360	365	
Val Pro Leu Asn His Leu Pro	Gly Met Pro Asp Thr His	Leu Gly Ile	
370	375	380	
Gly His Leu Asn Val Ala Ala Lys	Pro Glu Met Ala Ala	Leu Gly Gly	
385	390	395	400
Gly Gly Arg Leu Ala Phe Glu	Thr Gly Pro Pro Arg	Leu Ser His Leu	
405	410	415	
Pro Val Ala Ser Gly Thr Ser	Thr Val Leu Gly Ser	Ser Ser Gly Gly	
420	425	430	
Ala Leu Asn Phe Thr Val Gly	Gly Ser Thr Ser Leu Asn	Gly Gln Cys	
435	440	445	
Glu Trp Leu Ser Arg Leu Gln	Ser Gly Met Val Pro	Asn Gln Tyr Asn	
450	455	460	
Pro Leu Arg Gly Ser Val Ala	Pro Gly Pro Leu Ser	Thr Gln Ala Pro	
465	470	475	480
Ser Leu Gln His Gly Met Val	Gly Pro Leu His Ser	Ser Leu Ala Ala	
485	490	495	
Ser Ala Leu Ser Gln Met Met	Ser Tyr Gln Gly Leu	Pro Ser Thr Arg	
500	505	510	
Leu Ala Thr Gln Pro His Leu	Val Gln Thr Gln Gln	Val Gln Pro Gln	
515	520	525	
Asn Leu Gln Met Gln Gln	Asn Leu Gln Pro Ala	Asn Ile Gln Gln	
530	535	540	
Gln Gln Ser Leu Gln Pro	Pro Pro Pro Pro Gln	Pro His Leu Gly	
545	550	555	560
Val Ser Ser Ala Ala Ser Gly	His Leu Gly Arg Ser	Phe Leu Ser Gly	
565	570	575	
Glu Pro Ser Gln Ala Asp Val	Gln Pro Leu Gly Pro	Ser Ser Leu Ala	
580	585	590	
Val His Thr Ile Leu Pro Gln	Glu Ser Pro Ala	Leu Pro Thr Ser Leu	
595	600	605	
Pro Ser Ser Leu Val Pro	Pro Val Thr Ala Ala	Gln Phe Leu Thr Pro	
610	615	620	
Pro Ser Gln His Ser Tyr	Ser Ser Pro Val Glu	Asn Thr Pro Ser His	
625	630	635	640
Gln Leu Gln Val Pro Glu His	Pro Phe Leu Thr Pro	Ser Pro Glu Ser	
645	650	655	
Pro Asp Gln Trp Ser Ser Ser	Pro His Ser Asn Val	Ser Asp Trp	
660	665	670	
Ser Glu Gly Val Ser Ser Pro	Pro Pro Thr		
675	680		